

Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1. (Currently amended) A method for the analysis of methylated DNA as compared to background DNA of the same sequence but another methylation pattern comprising:

a) converting the DNA to be investigated is chemically or enzymatically so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base pairing behavior,

b) hybridizing the converted DNA with oligonucleotides, whereby the background DNA forms hybrids with erroneous base pairings,

c) cleaving the converted DNA strand of the erroneously paired hybrids enzymatically,

d) amplifying the uncleaved converted DNA,

e) detecting the amplicates,

f) concluding the methylation status of the investigated DNA from the detection signal generated in step e),

g) wherein steps b) through d) are conducted simultaneously.

2. (Canceled)

3. (Canceled)

4. (Canceled)

5. (Canceled)

6. (Previously presented) The method according to claim 1, wherein the background DNA forms several erroneous base pairings with the oligonucleotides.

7. (Currently amended) The method according to claim 1, wherein the oligonucleotides utilized in step b) are ~~also~~ simultaneously utilized as primers or probes in ~~a later~~ an amplification step.

8. (Canceled)

9. (Previously presented) The method according to claim 1, wherein the amplification or the detection of the amplicates is carried out in a methylation-specific manner.

10. (Previously presented) The method according to claim 1, wherein said amplifying step comprises amplifying several fragments simultaneously.

11. (Previously presented) The method according to claim 1, wherein the detection in step e) is made by means of a microarray.

12. (Previously presented) The method according to claim 1, wherein said cleaving step of step c) comprises utilizing a DNA repair enzyme.

13. (Previously presented) The method according to claim 12, wherein said DNA repair enzyme is selected from the group consisting of Mut Y, Mug protein, DNA glycosylase and TDG enzyme.

14. (Previously presented) The method according to claim 12, wherein said DNA repair enzyme is heat-stable.

15. (Previously presented) The method according to claim 13, wherein the TDG enzyme is heat-stable.

16. (Canceled)

17. (Currently amended) A method for the diagnosis or prognosis of cancer disorders or other diseases associated with a change in the cytosine methylation status, for predicting undesired drug interactions, for establishing a specific drug therapy, for monitoring the success of a drug therapy, for distinguishing cell types or tissues and for investigating cell differentiation, said method comprising analysis of methylated DNA as compared to background DNA of the same sequence but another methylation pattern, and further comprising the steps of:

a) converting the DNA to be investigated chemically or enzymatically so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base pairing behavior,

b) hybridizing the converted DNA with oligonucleotides, whereby the background DNA forms hybrids with erroneous base pairings,

c) cleaving the converted DNA strand of the erroneously paired hybrids enzymatically,

d) amplifying the uncleaved converted DNA,

e) detecting the amplificates,

f) using the detection signal generated in step e) to obtain a diagnosis or prognosis of cancer disorders or other diseases associated with a change in the cytosine methylation status, to predict undesired drug interactions, to establish a specific drug therapy, to monitor the success of a drug therapy, to distinguish cell types or tissues and to investigate cell differentiation,

g) wherein steps b) through d) are conducted simultaneously.

18. (Currently amended) A method for the early diagnosis of cancer disorders or other

diseases associated with a change in the cytosine methylation status, said method comprising analysis of methylated DNA as compared to background DNA of the same sequence but another methylation pattern, and further comprising comprising the steps of:

a) converting the DNA to be investigated chemically or enzymatically so that 5-methylcytosine remains unchanged, while unmethylated cytosine is converted to uracil or to another base which differs from cytosine in its base pairing behavior,

b) hybridizing the converted DNA with oligonucleotides, whereby the background DNA forms hybrids with erroneous base pairings,

c) cleaving the converted DNA strand of the erroneously paired hybrids enzymatically,

d) amplifying the uncleaved converted DNA,

e) detecting the amplicates,

f) using the detection signal generated in step e) for the early diagnosis of cancer disorders or other diseases associated with a change in the cytosine methylation status,

g) wherein steps b) through d) are conducted simultaneously.

19. (Previously presented) The method according to claim 1 further comprising the step of isolating the DNA to be investigated from a body fluid sample of an individual.

20. (Previously presented) The method according to claim 1 further comprising the step of isolating the DNA to be investigated from a serum, plasma, sperm, urine or stool sample of an individual.

21. (Canceled)

22. (Canceled)

23. (Canceled)